

FIGURE 1

Amino acid sequence for full-length human wild type FAP α [SEQ. ID No. 1]
(Residues 27-760 are underlined)

MKTWVKIVFG	VATSAVLALL	VMCIVL	<u>[(RPSR)]</u>	<u>RPSR</u>	VHNSEENTMR	ALTLDILNG	
<u>TFSYKTFFPN</u>							60
WISGQEYLHQ	SADNNIVLYN	IETGQSYTIL	SNRTMKSVNA	SNYGLSPDRQ	FVYLESDDYSK		120
LWRYSYTATY	YIYDLNNGEF	VRGNELPRPI	QYLCWSPVGS	KLAYVYQNNI	YLKQRPFGDPP		180
FQITFNGREN	KIFNGIPDWV	YEEMLATKY	ALWWSPNGKF	LAYAEFNDDT	IPVIAYSYYG		240
DEQYPRITNI	PYPKAGAKNP	VVRIFIIDTT	YPAYVGPQEV	PVPAMIASSD	YFWSLTWVT		300
DERVCLQWLK	RVQNVSVLSI	CDFREDWQTV	DCPKTQEHIE	ESRTGWAGGF	FVSTPVFSYD		360
AISYYKIFSD	KDGYKHIHYI	KDTVENAIQI	TSGKWEAINI	FRVTQDSLFI	SSNEFEEYPG		420
RRNIYRISIG	SYPPSKKCVT	CHLRKERCQY	YTASFSDYAK	YYALVCYGP	IPISTLHDGR		480
TDQEIKILEE	NKELENALKN	IQLPKKEIKK	LEVDEITLWY	KMILPPQFDR	SKKYPLLIQV		540
YGGPCSQSVR	SVFAVNWISY	LASKEGMVIA	LVDGRGTAFQ	GDKLLYAVYR	KLGVYEVEDQ		600
ITAVRKFIEM	GFIDEKRIAI	WGWSYGGYVS	SLALASGTGL	FKCGIAPVAP	SSWEYYASVY		660
TERFMGLPTK	DDNLEHYKNS	TVMARAEYFR	NVDYLLIHGT	ADDNVHVFQNS	AQIAKALVNA		720
QVDFQAMWYS	DQNHGLSGLS	TNHLTYHMT	FLKQCFSLSD				760

Amino acid sequence for residues 27-760 of FAP α with a
C-terminal 6x-histidine tag and a N-terminal signal sequence [SEQ. ID No. 3]
(6x-histidine C-terminal tag and signal sequence are underlined)

ADPGRPSRVH	NSEENTMRAL	TLKDILNGTF	SYKTFFPNWI	SGQEYLHQSA	DNNIVLYNIE		60
TGQSYTILSN	RTMKSVNASN	YGLSPDRQFV	YLESDDYSKLW	RYSYTATYYI	YDLNNGEFVR		120
GNELPRPIQY	LCWSPVGSKL	AYVYQNNIYL	KQRPDPPFFQ	ITFNGRENKI	FNGIPDWVYE		180
EEMLATKYAL	WWSPNGKFLA	YAEFNDDTIP	VIAYSYYGDE	QYPRITINIPY	PKAGAKNPVV		240
RIFIIDTTYP	AYVGPQEVVP	PAMIASSDYY	FSWLTWVTDE	RVCLQWLKRV	QNVSVLSICD		300
FREDWQTVDC	PKTQEHIEES	RTGWAGGFFV	STPVFSYDAI	SYKIFSDKD	GYKHIHYIKD		360
TVENAIQITS	GKWEAINIFR	VTQDSLFIYS	NEFEEYPGRR	NIYRISIGSY	PPSKKCVTCH		420
LRKERCQYYT	ASFSDYAKYY	ALVCYGP	IPISTLHDGR	TDQEIKILEENK	ELENALKNIQ		480
LPKEIKKLE	VDEITLWYKM	ILPPQFDRSK	KYPLLIQVYG	GPCSQSVRSV	FAVNWISYLA		540
SKEGMVIALV	DGRGTAFQGD	KLLYAVYRKL	GVYEVEDQIT	AVRKFIEMGF	IDEKRIAIWG		600
WSYGGYVSSL	ALASGTGLFK	CGIAPVAVSS	WEYYASVYTE	RFMGLPTKDD	NLEHYKNSTV		660
MARAEYFRNV	DYLLIHGTAD	DNVHVFQNSAQ	IAKALVNAQV	DFQAMWYSDQ	NHGLSGLSTN		720
HLTYHMTFL	KQCFSLSDHH	HHHH					744

FIGURE 3

LEGEND

Column headings from left to right are (A)'Atom Number', (B)'Atom Type', (C)'Amino Acid', (D)'Chain Identifier', (E)'Amino Acid Number' (SEQ. ID No. 1), (F)'X Coordinate', (G)'Y Coordinate', (H)'Z Coordinate', (I)'Occupancy' (OCC) and (J)'B factor'.

A	B	C	D	E	F	G	H	I	J
1	N	MET	A	39	5.996	-20.235	69.783	1.00	18.72
2	CA	MET	A	39	7.324	-20.790	69.338	1.00	19.11
3	CB	MET	A	39	7.346	-22.312	69.513	1.00	20.53
4	CG	MET	A	39	8.358	-22.796	70.590	1.00	24.21
5	SD	MET	A	39	9.670	-21.516	71.105	1.00	32.68
6	CE	MET	A	39	10.431	-22.591	72.605	1.00	28.08
7	C	MET	A	39	7.711	-20.442	67.883	1.00	18.40
8	O	MET	A	39	6.962	-20.696	66.950	1.00	18.52
9	N	ARG	A	40	8.884	-19.871	67.661	1.00	16.98
10	CA	ARG	A	40	9.131	-19.326	66.323	1.00	15.95
11	CB	ARG	A	40	8.357	-18.006	66.139	1.00	15.89
12	CG	ARG	A	40	9.195	-16.728	65.961	1.00	12.97
13	CD	ARG	A	40	8.391	-15.625	65.382	1.00	10.58
14	NE	ARG	A	40	8.571	-14.408	66.124	1.00	8.31
15	CZ	ARG	A	40	9.339	-13.389	65.717	1.00	9.61
16	NH1	ARG	A	40	10.025	-13.429	64.565	1.00	8.91
17	NH2	ARG	A	40	9.413	-12.317	66.478	1.00	7.17
18	C	ARG	A	40	10.576	-19.104	65.952	1.00	15.09
19	O	ARG	A	40	11.399	-18.790	66.791	1.00	14.36
20	N	ALA	A	41	10.836	-19.219	64.656	1.00	14.38
21	CA	ALA	A	41	12.120	-18.829	64.080	1.00	14.10
22	CB	ALA	A	41	12.368	-19.592	62.710	1.00	14.32
23	C	ALA	A	41	12.330	-17.265	63.949	1.00	13.47
24	O	ALA	A	41	11.382	-16.437	63.808	1.00	12.80
25	N	LEU	A	42	13.606	-16.902	64.046	1.00	12.98
26	CA	LEU	A	42	14.034	-15.508	63.901	1.00	12.60
27	CB	LEU	A	42	15.515	-15.320	64.228	1.00	12.38
28	CG	LEU	A	42	16.113	-15.110	65.616	1.00	10.25
29	CD1	LEU	A	42	17.663	-15.173	65.390	1.00	3.66
30	CD2	LEU	A	42	15.762	-13.787	66.312	1.00	5.75
31	C	LEU	A	42	13.791	-15.029	62.476	1.00	12.73
32	O	LEU	A	42	13.827	-15.769	61.502	1.00	11.78
33	N	THR	A	43	13.609	-13.735	62.390	1.00	13.33
34	CA	THR	A	43	13.086	-13.041	61.211	1.00	13.59
35	CB	THR	A	43	11.783	-12.404	61.712	1.00	14.28
36	OG1	THR	A	43	10.694	-13.134	61.178	1.00	15.37
37	CG2	THR	A	43	11.531	-10.976	61.322	1.00	11.61
38	C	THR	A	43	14.124	-12.063	60.852	1.00	14.41
39	O	THR	A	43	14.790	-11.603	61.742	1.00	15.57
40	N	LEU	A	44	14.371	-11.760	59.576	1.00	15.51
41	CA	LEU	A	44	15.348	-10.660	59.246	1.00	15.05
42	CB	LEU	A	44	15.599	-10.568	57.755	1.00	14.85

FIGURE 1

Amino acid sequence for full-length human wild type FAP α [SEQ. ID No. 1]

(Residues 27-760 are underlined)

<u>MKTWVKIVFG</u>	<u>VATSAVLALL</u>	<u>VMCIVLRPSR</u>	<u>VHNSEENTMR</u>	<u>ALTLKDILNG</u>	<u>TFSYKTFFPN</u>	60
<u>WISGQEYLHQ</u>	<u>SADNNIVLYN</u>	<u>IETGQSYTIL</u>	<u>SNRTMKSVNA</u>	<u>SNYGLSPDRQ</u>	<u>FVYLES DYSK</u>	120
<u>LWRYSYTATY</u>	<u>YIYDLSNGEF</u>	<u>VRGNELPRPI</u>	<u>QYLCWSPVGS</u>	<u>KLAYVYQNNI</u>	<u>YLKQRP GDPP</u>	180
<u>FQITFNGREN</u>	<u>KIFNGIPDWV</u>	<u>YEEEMLATKY</u>	<u>ALWWS PNGKF</u>	<u>LAYAEFNDTD</u>	<u>IPVIAYSYYG</u>	240
<u>DEQYPRTINI</u>	<u>PYPKAGAKNP</u>	<u>VVRIFIIDTT</u>	<u>YPAYVGPQEV</u>	<u>PVPAMIASSD</u>	<u>YYFSWLTWVT</u>	300
<u>DERVCLQWLK</u>	<u>RVQNVSVLSI</u>	<u>CDFREDWQTW</u>	<u>DCPKTQEHIE</u>	<u>ESRTGWAGGF</u>	<u>FVSTPVFSYD</u>	360
<u>AISYYKIFSD</u>	<u>KDGYKHIHYI</u>	<u>KDTVENAIQI</u>	<u>TSGKWEAINI</u>	<u>FRVTQDSL FY</u>	<u>SSNEFEEY PG</u>	420
<u>RRNIYRISIG</u>	<u>SYPPSKKCVT</u>	<u>CHLRKERCQY</u>	<u>YTASFSDYAK</u>	<u>YYALVCY GPG</u>	<u>IPISTLHDGR</u>	480
<u>TDQEI KILEE</u>	<u>NKELENALKN</u>	<u>IQLPKKEIKK</u>	<u>LEVDEITLWY</u>	<u>KMILPPQFDR</u>	<u>SKKYPLLIQV</u>	540
<u>YGGPCSQS VR</u>	<u>SVFAVNWISY</u>	<u>LASKEGMVIA</u>	<u>LVDGRGTAFQ</u>	<u>GDKLLYAVYR</u>	<u>KLGVYEVEDQ</u>	600
<u>ITAVRKFIEM</u>	<u>GFI DEKRIAI</u>	<u>WGWSYGGYVS</u>	<u>SLALASGTGL</u>	<u>FKCGI AVAPV</u>	<u>SSWEYYASVY</u>	660
<u>TERFMGLPTK</u>	<u>DDNLEHYKNS</u>	<u>TVMARAEYFR</u>	<u>NVDYLLIHGT</u>	<u>ADDNVH FQNS</u>	<u>AQIAKALVNA</u>	720
<u>QVDFQAMWYS</u>	<u>DQNHGLSGLS</u>	<u>TNHL YTHMTH</u>	<u>FLKQCFSLSD</u>			760

Amino acid sequence for residues 27-760 of FAP α with a

C-terminal 6x-histidine tag and a N-terminal signal sequence [SEQ. ID No. 3]

(6x-histidine C-terminal tag and signal sequence are underlined)

<u>ADPGRPSRVH</u>	<u>NSEENTMRAL</u>	<u>TLKDILNGTF</u>	<u>SYKTFFPNWI</u>	<u>SGQEYLHQSA</u>	<u>DNMIVLYNIE</u>	60
<u>TGQSYTILSN</u>	<u>RTMKSVNASN</u>	<u>YGLSPDRQFV</u>	<u>YLES DYSKLW</u>	<u>RYSYTATYYYI</u>	<u>YDLSNGEFVR</u>	120
<u>GNELPRPIQY</u>	<u>LCWSPVGSKL</u>	<u>AYVYQNNIYL</u>	<u>KQRPGDPPFQ</u>	<u>ITFNGRENKI</u>	<u>FNGIPDWVYE</u>	180
<u>EEMLATKYAL</u>	<u>WWS PNGKFLA</u>	<u>YAEFNDTDIP</u>	<u>VIAYSYYGDE</u>	<u>QYPRTINIPY</u>	<u>PKAGAKNPVV</u>	240
<u>RIFIIDTTYP</u>	<u>AYVGPQEV PV</u>	<u>PAMIASSDYY</u>	<u>FSWLTWVTDE</u>	<u>RVCLQWLKRV</u>	<u>QNVSVLSICD</u>	300
<u>FREDWQTWDC</u>	<u>PKTQEHIEES</u>	<u>RTGWAGGFFV</u>	<u>STPVFSYDAI</u>	<u>SYKIFSDKD</u>	<u>GYKHIHYIKD</u>	360
<u>TVENAIQITS</u>	<u>GKWEAINIFR</u>	<u>VTQDSL FYSS</u>	<u>NEFEEY PGRR</u>	<u>NIYRISIGSY</u>	<u>PPSKKCVTCH</u>	420
<u>LRKERCQYYT</u>	<u>ASFSDYAKYY</u>	<u>ALVCY GPGIP</u>	<u>ISTLHDGR TD</u>	<u>QEI KILEENK</u>	<u>ELENALKNIQ</u>	480
<u>LPKEEIKKLE</u>	<u>VDEITLWYKM</u>	<u>ILPPQFDRSK</u>	<u>KYPLLIQVYG</u>	<u>GPCSQS VRSV</u>	<u>FAVNWISYLA</u>	540
<u>SKEGMVIALV</u>	<u>DGRGTAFQGD</u>	<u>KLLYAVYRKL</u>	<u>GVYEVEDQIT</u>	<u>AVRKFIEMGF</u>	<u>IDEKRIAIWG</u>	600
<u>WSYGGYVSSL</u>	<u>ALASGTGLFK</u>	<u>CGI AVAPVSS</u>	<u>WEYYASVYTE</u>	<u>RFMGLPTKDD</u>	<u>NLEHYKNSTV</u>	660
<u>MARAEYFRNV</u>	<u>DYLLIHGTAD</u>	<u>DNVH FQNSAQ</u>	<u>IAKALVNAQV</u>	<u>DFQAMWYS DQ</u>	<u>NHGLSGLSTN</u>	720
<u>HLYTHMTHFL</u>	<u>KQCFSLS DHH</u>	<u>HHHH</u>				744

FIGURE 3

LEGEND

Column headings from left to right are (A)'Atom Number', (B)'Atom Type', (C)'Amino Acid', (D)'Chain Identifier', (E)'Amino Acid Number' (SEQ. ID No. 1), (F)'X Coordinate', (G)'Y Coordinate', (H)'Z Coordinate', (I)'Occupancy' (OCC) and (J)'B factor'.

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38	C	THR	A	43	14.124	-12.063	60.852	1.00	14.41
39	O	THR	A	43	14.790	-11.603	61.742	1.00	15.57
40	N	LEU	A	44	14.371	-11.760	59.576	1.00	15.51
41	CA	LEU	A	44	15.348	-10.660	59.246	1.00	15.05
42	CB	LEU	A	44	15.599	-10.568	57.755	1.00	14.85